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| Sequence 1112, Ap Sequence 1113, Ap Sequence 845, App Sequence 2244, Ap Sequence 845, App Sequence 2047, Ap | equence 174, Ap equence 171, Ap equence 174, Ap equence 7, Appl | equence 70, App | equence 7, Applequence 623, Ap | equence 93 | equence 491, Ap equence 511, Ap | equence 1137, A equence 1157, A | 84, App | 5 5 | 2296 | 6624 | 5029 | 503, | 3143 | 3143 | 1578 | 8044 | ιψα | 1852 | 5736 | 2293 | 2296 | 6624 | 4.0 | 2168 | 2168 | 487 | 113 | 922 | 224 | 314 | 3143 | 612 | 612 | 612 | 5735 | 283, | 0 0 |
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RESULT 4

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Sequence 1097, Application US/08985162

Sequence 1097, Application US/08985162

Patent No. 6057156

APPLICANT: Rell, Patricia

APPLICANT: McSwigen, James

TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED

TITLE OF INVENTION: TO LEVELS OF PRIDERMAL GROWTH

TITLE OF INVENTION: PACTOR RECEPTORS

NUMBER OF SEQUENCES:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STATE: Callifornia

COUNTRY: U.S.A
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Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 23; Conservative 0; Mismatches
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1.4%; Score 21.8; Di
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ORGANISM: Artificial Sequence
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
! LENGTH: 23
; TYPE: DNA
; ORGANISM: human
US-09-165-042-30
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Sequence 67, Appl
Sequence 738, Appl
Sequence 739, Appl
Sequence 1771, Appl
Sequence 1772, Appl
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Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 25, Application US/09165042

Patent No. 6100077

GENERAL INFORMATION;

APPLICANT: Sturiey, Stephen L.

APPLICANT: Ocikers, Peter

TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL

TITLE OF INVENTION: ACTUFRANSFERASE

FILE REFERENCE: 0575/56331

CURRENT APPLICATION NUMBER: US/09/165,042

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 32

CURRENT FILING DATE: PatentIN Ver. 2.0

SEQ ID NO 25

LENGTH: 25

TENGTH: 25

CRANISM: human

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       Patent No.
Patent No.
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US-09-165-042-30
Sequence 30, Application US/09165042
Sequence 30, Application US/09165042
Patent No. 6100077
GENERAL INFORMATION:
APPLICANT: Sturiey, Stephen L.
TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
TITLE OF INVENTION: ACYLTRANSFERASE
TITLE OF INVENTION: ACYLTRANSFERASE
TITLE OF INVENTION: ACYLTRANSFERASE
TITLE OF INVENTION: ACYLTRANSFERASE
CURRENT APPLICATION NUMBER: US/09/165,042
CURRENT APPLICATION DATE: 1998-10-01
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1.5%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 24; Conservative 0; Mismatches 0; Indels
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US-08-435-350-95

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US-08-88-684B-739

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GENERAL INFORMATION:
APPLICANT: Pan, Jian Bing
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TITLE OF INVENTION: Hypertension
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FILE OF INVENTION UNMBER: US/09/304,232
CURRENT APPLICATION NUMBER: US/09/304,641
EARLIER PILICATION NUMBER: US 60/084,641
EARLIER FILENG DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 909
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 29
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The present invention relates to novel antisense oligonucleotides which are targeted to human acyl CoA cholesterol acyltransferase-2 (ACAT-2) mucleotide sequence (ACC42409-ACC42431).

ACC42457). The antisense oligonucleotides specifically hybridise with and inhibit the expression of ACAT-2 nucleotide sequences (ACC42395 and ACC42402). ACAT enzymes catalyse the synthesis of cholesterol esters from free cholesterol and fatty acyl-CoA. The antisense oligonucleotides are useful for treating an animal which has a disease or condition associated with ACAT-2. e.g. a condition involving abnormal lipid metabolism, a condition involving abnormal cholesterol metabolism, atherosclerosis, or cardiovascular disease. The present sequence is a PCR probe for human ACAT-2, used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ACAT Related Gene Product 2; ARGP2; enzyme;
acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a human diacylglycerol acyltransferase, useful for treating hyperlipidemia, atherosclerosis, heart disease, or other diseases associated with an imbalance of triglyceride levels.
                                                 New antisense oligonuclectides for modulating acyl CoA cholesterol acyltranáferasez, e.g. for preventing or treating diseases associated with abnormal lipid or cholesterol metabolism, atherosclerosis, cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 4 A; 5 C; 10 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTACGTGTATCAGGATGGGCTGCGG 25
                                                                                                                                        Example 13; Page 85; 112pp; English.
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Matches 25; Conserv
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The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1) mediates sterol esterification, an important component of intracellular lipid

Disclosure; Col 17; 32pp; English.

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